Claim 6 (Amended). The method of [any one of the preceding claims] claim 1 wherein the breed determinant gene analysed in step (ii) is selected from [any of] the group consisting of:

(a) a coat [colour] color gene; [and/or]

(b) a coat pattern gene; [and/or]

(c) a coat texture gene; [and/or]

(d) a coat density gene; [and/or]

(e) a coat length gene; [and/or]

(f) an ear aspect gene; [and/or]

(g) a double muscling gene; [and/or]

(h) a horn morphology gene; [and/or]

(i) a tusk morphology gene; [and/or]

(j) an eye [colour] color gene; [and/or]

(k) a plumage gene; [and/or]

(l) a beak [colour] color/morphology gene; [and/or]

(m) a vocalization (e.g. barking) gene; [and/or]

(n) a comb or wattle gene; [and/or]

(o) a gene controlling display behaviour[.]; and

(p) combinations thereof.

Claim 7 (Amended). The method of claim 6[(a)] wherein the coat [colour] color gene is the *KIT* or *αMSHR* gene [(for example, the pig *KIT* or *αMSHR* gene)].

Claim 8 (Amended). The method [of any one of the preceding claims] of claim 1 wherein the sample is a nucleic acid sample and the analysing step (ii) comprises DNA or RNA analysis.

Claim 9 (Amended). The method of [any one of claims 1-7] claim 1 wherein the sample is a protein sample and the analysing step (ii) comprises protein analysis.

Claim 10 (Amended). A method of determining the coat [colour] color genotype of a pig which comprises:

(i) obtaining a sample of pig nucleic acid; and

(ii) analysing the nucleic acid obtained in (i) to determine which [allele or] alleles of the [αMSHR] αMSHR gene [is/] are present.

Claim 11 (Amended). The method of claim 8 [or claim 10] wherein the analysis step (ii) [comprises] is selected from the group consisting of:

(a) selectively amplifying a specific fragment of nucleic acid [(e.g. by PCR); and/or]:

(b) testing for the presence of one or more restriction endonuclease sites within the breed determinant gene(s)[/αMSHR gene (e.g., restriction fragment length polymorphism (RFLP) analysis); and/or]:

(c) determining the nucleotide sequence of all or a portion of the breed determinant gene(s)[/αMSHR gene; and/or]:

(d) probing the nucleic acid sample with an allele-specific DNA or RNA probe; [and/or]:

(e) carrying out one or more PCR amplification cycles of the nucleic acid sample using at least one pair of suitable primers and then carrying out RFLP analysis on the amplified nucleic acid so obtained; and

(f) combinations thereof.

Claim 12, line 4, delete "colour" and insert --color--;

line 5, after "protein" insert --.--.

Claim 13 (Amended). The method of claim [9 or claim] 12 wherein the analysis step (ii) [comprises] is selected from the group consisting of:

(a) probing the protein sample with an antibody [(e.g. a monoclonal antibody)] specific for an allele-specific epitope; [and/or]

(b) electrophoretic analysis; [and/or]

(c) chromatographic analysis; [and/or]

(d) amino-acid sequence analysis; [and/or]

(e) proteolytic cleavage analysis; [and/or]

(f) epitope mapping; [and/or]

(g) translating a copy of the DNA or RNA of the gene produced by PCR or other means in an in-vitro transcription/translation system; and

(h) combinations thereof.

Claim 15, line 1, delete "or claim 14".

Claim 16, line 1, delete "or claim 11".

Claim 17 (Amended). The method of [any one of claims] claim 7[, 10, 11, 14 and 15] wherein the analysis step (ii) further comprises determining the association between one or

more microsatellite or other linked marker alleles linked to the *KIT* or *αMSHR* gene and to particular alleles of the *KIT* or *αMSHR* gene.

Claim 19, line 1, delete "7" and insert --17--; and

line 5, delete "allele or".

Claim 20, line 1, delete "colour" and insert --color--; and

line 7, delete "allele or".

Claim 21, line 1, delete "any one of claims 7, 10, 11 and 14-20" and insert --claim 7--.

Claim 22, line 1, delete "colour" and insert --color--.

Claim 23 (Amended). The method of claim 22 wherein the additional coat [colour] color locus is the *KIT* gene locus [(e.g. the pig *KIT* gene locus)].

Claim 26, line 1, delete "colour" and insert --color--.

Claim 28 (Amended). A method as claimed in claim 26 [or claim 27 wherein a sample of pig] wherein said pig nucleic acid is genomic DNA [is amplified] and further comprising the step of amplifying said genomic DNA using PCR and a pair of suitable primers.

Claim 29 (Amended). The method of claim 21 wherein the additional locus is a breed determinant gene locus [selected from any of those genes specified in claim 6] selected from the group consisting of:

(a) a coat color gene;

(b) a coat pattern gene;

(c) a coat texture gene;

(d) a coat density gene;

(e) a coat length gene;

(f) an ear aspect gene;

(g) a double muscling gene;

(h) a horn morphology gene;

(i) a tusk morphology gene;

(j) an eye color gene;

(k) a plumage gene;

(l) a beak color/morphology gene;

(m) a vocalization (e.g. barking) gene;

(n) a comb or wattle gene;

(o) a gene controlling display behaviour; and

(p) combinations thereof.

Claim 32 (Amended). The method of [any one of claims] claim 7[, 10, 11, 14-23 and 28-31] wherein the analysis step (ii) comprises PCR using at least one pair of suitable primers.

Claim 33 (Amended). The method of claim 32 wherein the gene is the pig *αMSHR* gene and at least one pair of suitable primers is selected from the group consisting of:

[αMSHR] *αMSHR* Forward Primer 1: (5'-TGT AAA ACG ACG GCC AGT RGT GCC TGG AGG TGT-3');

[αMSHR] *αMSHR* Reverse Primer 5: (5'-CGC CCA GAT GGC CGC GAT GGA CCG-3'); [or]

[αMSHR] *αMSHR* Forward Primer 2: (5'-CGG CCA TCT GGG CGG GCA GCG TGC-3')

[αMSHR] _αMSHR_ Reverse Primer 2: (5'-GGA AGG CGT AGA TGA GGG GGT CCA-3'); [or]

and

[αMSHR] _αMSHR_ Forward Primer 3: (5'-GCA CAT CGC CCG GCT CCA CAA GAC-3')

[αMSHR] _αMSHR_ Reverse Primer 3: (5'-GGG GCA GAG GAC GAC GAG GGA GAG-3').

Claim 34 (Amended). The method of [any one of claims 7, 10, 11, 14-23 and 28-33] _claim 10_ wherein the analysis step (ii) comprises restriction fragment length polymorphism (RFLP) analysis [for example involving digesting the pig nucleic acid with one or more of the restriction enzymes _Bst_UI, _Hha_I and/or _Bsp_HI].

Claim 35, line 4, delete "1010of" and insert -- 1010 of--.

Claim 37 (Amended). The method of claim 36 wherein the gene is the pig _αMSHR_ gene and the at least one pair of suitable primers is as [defined in claim 35] selected from the group consisting of:

αMSHR Forward Primer 1: (5'-TGT AAA ACG ACG GCC AGT RGT GCC TGG AGG TGT -3');

αMSHR Reverse Primer 5: (5'-CGC CCA GAT GGC CGC GAT GGA CCG-3');

αMSHR Forward Primer 2: (5'-CGG CCA TCT GGG CGG GCA GCG TGC-3')

αMSHR Reverse Primer 2: (5'-GGA AGG CGT AGA TGA GGG GGT CCA-3'); and

αMSHR Forward Primer 3: (5'-GCA CAT CGC CCG GCT CCA CAA GAC-3')

αMSHR Reverse Primer 3: (5'-GGG GCA GAG GAC GAC GAG GGA GAG-3').

Claim 38 (Amended). The method of claim 30 [or 31] wherein the gene is the pig *KIT* or *αMSHR* gene and the <u>determination step comprises</u> RFLP analysis [is as defined in claim 28] <u>in which pig genomic DNA is amplified using PCR and a pair of suitable primers</u>.

Claim 39 (Amended). The method of [any one of claims 1-9, 11, 13-19, 21-25 and 29-38] <u>claim 1</u> wherein the animal product is <u>selected from the group consisting of</u> meat [(e.g., processed and/or canned meat)], egg, egg swab or washing, semen, wool [or] <u>and</u> leather.

Claim 40 (Amended). The method of [any one of claims 1-9, 11, 13-19 and 21-39] <u>claim 1</u> wherein the sample comprises genomic DNA, RNA or mitochondrial DNA.

Claim 41 (Amended). The method of [any one of claims 1-9, 11, 13-19 and 21-40] <u>claim 1</u> wherein the animal is <u>selected from the group consisting of</u> [a] mammal [(e.g. pig, cattle, dog, cat, horse, sheep rodent or rabbit)], fish [(e.g. salmon or trout) or] <u>and</u> bird [(chicken or turkey)].

Claim 43, line 1, delete "colour" and insert --color--.

Claim 44, line 1, delete "claim 42 or".

Claim 45 (Amended). A kit as claimed in [any on of claims 42 to 44] <u>claim 43</u> comprising one or more reagents for carrying out at least one cycle of PCR together with at least one pair of suitable primers.

Claim 46 (Amended). A kit as claimed in claim 45 wherein the [atleast] <u>at least</u> one pair of suitable primers is <u>selected from the group consisting of</u>:

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[αMSHR] *αMSHR* Forward Primer 1: (5'-TGT AAA ACG ACG GCC AGT RGT GCC TGG AGG TGT CCA T-3')

[αMSHR] *αMSHR* Reverse Primer 5: (5'-CGC CCA GAT GGC CGC GAT GGA CCG-3'); [or]

[αMSHR] *αMSHR* Forward Primer 2: (5'-CGG CCA TCT GGG CGG GCA GCG TGC-3')

[αMSHR] *αMSHR* Reverse Primer 2: (5'-GGA AGG CGT AGA TGA GGG GGT CCA-3'); [or] and

[αMSHR] *αMSHR* Forward Primer 3: (5'-GCA CAT CGC CCG GCT CCA CAA GAC-3')

[αMSHR] *αMSHR* Reverse Primer 3: (5'-GGG GCA GAG GAC GAC GAG GGA GAG-3').

Claim 47 (Amended). A kit as claimed in [any one of claims 42 to 46] claim 42 which comprises one or more reagents for RFLP analysis of pig nucleic acid.

Please add the following new claims:

-- 48. The method of claim 34 wherein said RFLP analysis comprises digesting pig nucleic acid with a restriction enzyme selected from the group consisting of *Bst*UI, *Hha*I, *Bsp*HI and mixtures thereof.

49. The method of claim 39 wherein said meat is selected from the group consisting of processed meat, canned meat, and mixtures thereof.

50. The method of claim 41 wherein said mammal is selected from the group consisting of pig, cattle, dog, cat, horse, sheep, rodent and rabbit, said fish is selected from the group consisting of salmon and trout, and said bird is selected from the group consisting of chicken and turkey. --